

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:33:36 : Search time 176 Seconds

(without alignments)
480.074 Million cell updates/sec

Title: US-09-786-867C-5

Perfect score: 893

Sequence: 1 MTTASTSQVRQNYHQDSEAA.....PRRKPKHSIPTPILFRSP 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

1612378

Minimum DB Seq length: 0

Maximum DB Seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : UniProt 03:*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	890	99.7	165	Q8TD27 homo sapien
2	615	68.9	2 Q6NS36	Q6ns36 homo sapien
3	610.5	68.4	182	1 FRTH_HUMAN
4	605.5	67.8	183	2 Q6NZ44
5	589.5	66.0	182	1 FRTH_TRIVU
6	589.5	66.0	183	2 Q9SMF7
7	586.5	65.7	182	2 Q92OK4
8	585	65.5	197	2 Q6SPV2
9	583.5	65.3	220	2 Q6GHIS
10	583.5	65.3	229	2 Q6AYV6
11	580	65.0	185	1 FRTH_CRIGR
12	575.5	64.4	181	1 FRTH_MOUSE
13	573.5	64.2	181	1 FRTH_RAT
14	570.5	63.9	182	2 Q8M1P0
15	560.5	62.8	170	1 FRTH_SHEBP
16	560.5	62.8	179	1 FRTH_CHICK
17	560.5	62.8	180	1 FRTH_BOVIN
18	560.5	62.8	181	2 Q6PRTV1
19	516.5	57.8	177	2 Q72XMB
20	515.5	57.7	177	2 Q6DBBS
21	514.5	57.6	169	2 QBH2P4
22	514.5	57.6	177	1 FRH3_XENIA
23	508.5	56.9	180	1 FRTH_PIG
24	500	56.0	157	2 Q7ZBT8
25	499.5	55.9	164	1 FRTH_RABIT
26	494	55.3	100	2 Q862J4
27	494	55.3	242	2 Q8NAE7
28	488.5	54.7	152	2 Q6EEB2
29	480	53.8	132	2 Q61241
30	479	53.6	237	2 Q9DFP4
31	477	53.4	262	2 Q9D5H4

32	475	53.2	177	1 FRTH_SALSA
33	469	52.5	177	2 Q9DDT0
34	460.5	51.6	175	2 Q801J6
35	458	51.3	177	2 Q66IX7
36	457	51.2	92	2 Q862DS
37	456.5	51.1	127	2 Q862RA
38	453	50.7	176	2 Q98TTO
39	441	49.4	156	2 Q6EB31
40	440	49.3	177	2 Q801JS
41	439	49.2	173	1 FRIS_LYMST
42	436	48.8	134	2 Q86QN8
43	436	48.8	172	2 Q6WWN7
44	435.5	48.8	149	2 Q9GNC9
45	435.5	48.8	174	2 Q861LZ3

ALIGNMENTS

RESULT 1		PRELIMINARY;		PRT;		165 AA.	
ID	Q8TD27	ID	Q8TD27	ID	Q8TD27;	SEQUENCE FROM N.A.	
AC		AC		AC		MEDLINE=21935397; PubMed=112121435; DOI=10.1074/jbc.M200956200;	
DT		DT		DT		MOTZC, Traub L., Maymon R., Zahalka M.A.;	
DT		DT		DT		"PLIF, a novel human ferritin subunit from placenta with PLIF, a novel human ferritin subunit from placenta with	
DE		DE		DE		immunosuppressive activity";	
OS		OS		OS		J. Biol. Chem. 277:12901-12905 (2002).	
OU		OU		OU		-i SIMILARITY: Belongs to the ferritin family.	
RN		RN		RN		-i SIMILARITY: Contains 1 ferritin-like domain.	
CC		CC		CC		DR EMBL; AY033611; AAK55486.1; - .	
DR		DR		DR		HSSP P02794; 2 PHA.	
DR		DR		DR		GO; GO:0005886; C: plasma membrane; NAS.	
DR		DR		DR		GO; GO:0019900; C: kinase binding; NAS.	
DR		DR		DR		GO; GO:0006955; C: immune response; IDA.	
DR		DR		DR		InterPro; IPR00285; Pinnegative regulation of cell proliferation; IDA.	
DR		DR		DR		InterPro; IPR001519; Ferritin.	
DR		DR		DR		InterPro; IPR009078; Ferritin/RR like.	
DR		DR		DR		InterPro; IPR00331; Ferritin_Dps.	
DR		DR		DR		InterPro; IPR009040; Ferritin_1.	
DR		DR		DR		Pfam; PF00210; Ferritin_1.	
DR		DR		DR		ProDom; PD000911; Ferritin_1.	
DR		DR		DR		PROSITE; PS00540; FERRITIN_1.	
DR		DR		DR		PROSITE; PS50305; FERRITIN_LIKE.	
KW		KW		KW		Iron_Iron storage_Metal-Binding	
SEQUENCE		SEQUENCE		SEQUENCE		19490 MW; C4849C853FCABAB6 CRC64;	
Query Match		Query Match		Query Match		99.7%; Score 890; DB 2;	
Best Local Similarity		Best Local Similarity		Best Local Similarity		99.4%; Pred. No. 1.1e-71;	
Matches		Matches		Matches		1; Mismatches 0; Indels 0; Gaps 0;	

1 MTTASTATSVQRNYHODSEAANRQINLEYASYYVLSMSYFDRDDVALKNFAKYFLHQ5 60

1 MTTASTATSVQRNYHODSEAANRQINLEYASYYVLSMSYFDRDDVALKNFAKYFLHQ5 60

1 HEERHAEKLMKLQNQRGGRIPFLDKIKPCDDWGSNAMECAHLKVNOSLLEFPS 120

61 HEERHAEKLMKLQNQRGGRIPFLDKIKPCDDWGSNAMECAHLKVNOSLLEFPS 120

61 HEERHAEKLMKLQNQRGGRIPFLDKIKPCDDWGSNAMECAHLKVNOSLLEFPS 120

121 PISPSSCSWHYHTTNRQPQPHLLRPRRGRPHSIFTPLLFRSP 165

121 PISPSSCSWHYHTTNRQPQPHLLRPRRGRPHSIFTPLLFRSP 165